

CLAIMS

1 1. An apparatus comprising:
2 a sequence database configured to contain entries of sequences;
3 a sequence comparitor configured to receive a patient sample sequence, to
4 compare the patient sample sequence with entries in the sequence database
5 to determine closest matches, and to normalize a matching score of the
6 closest matches.

1 2. The apparatus of claim A1, wherein the sequence comparitor is further
2 configured to determine whether the matching score of the closest matches
3 are within a confidence threshold.

1 3. The apparatus of claim A2 further comprising:
2 a patient profile manager to reporting whether a sample patient identifier
3 associated with the patient sample sequence matches a matched patient
4 identifier associated with the closest match;

1 4. The apparatus of claim A3 wherein the patient sample sequence is
2 sequenced from a virus.

1 5. The apparatus of claim A4 wherein the virus is hepatitis or Human
2 Immunodeficiency Virus (HIV).

1 6. The apparatus of claim A3 wherein the patient sample sequence is
2 sequenced from deoxyribonucleic acid (DNA).

1 7. The apparatus of claim A5 wherein the confidence threshold is
2 approximately three standard deviations from an average normalized
3 score.

1 8. A method comprising:

2 receiving a patient sample sequence, the patient sample sequence being associated
3 with a sample patient identifier;
4 comparing the patient sample sequence with entries in a sequence database to
5 determine closest matches, the closest matches being associated with a
6 matched patient identifier;
7 normalizing a matching score of the closest matches.

1 9. The method of claim 8 further comprising:
2 determining whether the matching score of the closest matches are within a
3 confidence threshold.

1 10. The method of claim 9 further comprising:
2 reporting the closest matches within the confidence threshold.

1 11. The method of claim 9 further comprising:
2 reporting whether the sample patient identifier matches the matched patient
3 identifier;

1 12. The method of claim 11 wherein the patient sample sequence is sequenced
2 from a virus.

1 13. The method of claim 12 wherein the virus is hepatitis or Human
2 Immunodeficiency Virus (HIV).

1 14. The method of claim 10 wherein the patient sample sequence is sequenced
2 from deoxyribonucleic acid (DNA).

1 15. The method of claim 13 wherein the confidence threshold is approximately
2 three standard deviations from an average normalized score.

1 16. A computer-readable medium encoded with data and instructions, the data
2 and instructions causing an apparatus executing the instructions to:

3 receive a patient sample sequence, the patient sample sequence being associated
4 with a sample patient identifier;
5 compare the patient sample sequence with entries in a sequence database to
6 determine closest matches, the closest matches being associated with a
7 matched patient identifier;
8 normalize a matching score of the closest matches.

1 17. The computer-readable medium of claim 16 wherein the instruction further
2 causes an apparatus to:

3 determine whether the matching score of the closest matches are within a
4 confidence threshold.

1 18. The computer-readable medium of claim 17 wherein the instruction further
2 causes an apparatus to:

3 report the closest matches within the confidence threshold.

1 19. The computer-readable medium of claim 18 wherein the instruction further
2 causes an apparatus to:

3 report whether the sample patient identifier matches the matched patient identifier;

1 20. The computer-readable medium of claim 19 wherein the patient sample
2 sequence is sequenced from a virus.

1 21. The computer-readable medium of claim 20 wherein the virus is hepatitis
2 or Human Immunodeficiency Virus (HIV).

1 22. The computer-readable medium of claim 18 wherein the patient sample
2 sequence is sequenced from deoxyribonucleic acid (DNA).

1 23. The computer-readable medium of claim 21 wherein the confidence
2 threshold is approximately three standard deviations from an average
3 normalized score.

1 24. An apparatus comprising:
2 means for receiving a patient sample sequence, the patient sample sequence being
3 associated with a sample patient identifier;
4 means for comparing the patient sample sequence with entries in a sequence
5 database to determine closest matches, the closest matches being
6 associated with a matched patient identifier;
7 means for normalizing a matching score of the closest matches.

1 25. The apparatus of claim 24 further comprising:
2 means for determining whether the matching score of the closest matches are
3 within a confidence threshold.

1 26. The apparatus of claim 25 further comprising:
2 means for reporting the closest matches within the confidence threshold.

1 27. The apparatus of claim 26 further comprising:
2 means for reporting whether the sample patient identifier matches the matched
3 patient identifier;

1 28. The apparatus of claim 27 wherein the patient sample sequence is
2 sequenced from a virus.

1 29. The apparatus of claim 28 wherein the virus is hepatitis or Human
2 Immunodeficiency Virus (HIV).

1 30. The apparatus of claim 26 wherein the patient sample sequence is
2 sequenced from deoxyribonucleic acid (DNA).

1 31. The apparatus of claim 29 wherein the confidence threshold is
2 approximately three standard deviations from an average normalized
3 score.